the wheat-*Aegilops* homoeologous relationships between the examined *Aegilops* chromosomes. The selection of wheat–*Aegilops* homoeologous recombinations could be successful in later generations.

Molecular cytogenetic evaluation of chromosome instability in *T. aestivum–S. cereale* disomic addition lines. The genetic stability of wheat–rye (Chinese Spring–Imperial) disomic addition lines was checked using the Feulgen method and FISH. Feulgen staining detected varying proportions of disomic, monosomic, and telosomic plants among the progenies of the disomic addition lines. The greatest stability was observed for the 7R addition line, whereas the most unstable lines were those with 2R and 4R additions. Chromosome rearrangements also were detected using FISH. Based on the specific hybridization patterns of repetitive DNA probes pSc119.2 and (AAC)5, as well as ribosomal DNA probes (5S and 45S), isochromosomes were identified in the progenies of 1R and 4R addition lines. These results draw attention to the importance of continuous cytological checks on basic genetic materials by using FISH, because this method reveals chromosome rearrangements that could not be detected either with the conventional Feulgen staining technique or with molecular markers.

Selection of U and M genome-specific wheat SSR markers using wheat–*Ae. biuncialis* and wheat–*Ae. geniculata* addition lines. Wheat SSR markers specific to the U and M genomes of *Aegilops* species were selected. A total of 108 wheat SSR markers were successfully tested on *Ae. biuncialis* (2n = 4x = 28, $U^bU^bM^bM^b$), on five wheat–*Ae. biuncialis* addition lines ($2M^b$, $3M^b$, $7M^b$, $3U^b$, and $5U^b$) and on a wheat–*Ae. geniculata* ($1U^g$, $2U^g$, $3U^g$, $4U^g$, $5U^g$, $7U^g$, $1M^g$, $2M^g$, $4M^g$, $5M^g$, $6M^g$, and $7M^g$) addition series. Among the markers, 86 (79.6%) were amplified in the *Ae. biuncialis* genome. Compared with wheat, polymorphic bands of various lengths were detected in *Ae. biuncialis* for 35 (32.4%) of the wheat microsatellite markers. Three of these (8.6%) exhibited specific PCR products in wheat–*Ae. biuncialis* or wheat–*Ae. geniculata* addition lines. The primers GWM44 and GDM61 gave specific PCR products in the $2M^b$ and $3M^b$ wheat–Ae. biuncialis addition lines, but not on the $2M^g$ addition line of *Ae. geniculata*. A specific band was observed on the $7U^g$ wheat–*Ae. geniculata* addition line using the BARC184 primer. T hese three markers specific to the U and M genomes are helpful for the identification of $2M^b$, $3M^b$, and $7U^g$ chromosome introgressions into wheat.

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ITEMS FROM INDIA

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Application of Real-Time PCR in marker-assisted selection for stem rust resistance gene Sr24.

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Introduction. Real-Time PCR (RT–PCR) is a technique mainly used to amplify and simultaneously quantify a targeted DNA molecule (Gibson et al. 1996). Currently, four different chemistries, TaqMan® (Applied Biosystems, Foster City, CA, USA); Molecular Beacons (Newark, New Jersey, USA); Scorpions® (Sigma-Aldrich, St. Louis, MO, USA); and SYBR® Green (Life Technologies, Carlsbad, CA, USA), are available for RT-PCR. All of these chemistries allow

detection of PCR products via the generation of a fluorescent signal. Among the SYBR Green is a fluorogenic dye that exhibits little fluorescence when in solution, but emits a strong fluorescent signal upon binding to double-stranded DNA (Arya et al. 2005).

Real-time PCR can be applied to traditional PCR applications as well as new applications that would have been less effective with traditional PCR. With the ability to collect data in the exponential growth phase, the power of PCR has been expanded into applications such as viral quantitation, quantitation of gene expression, array verification, drug therapy efficacy, DNA damage measurement, quality control and assay validation, pathogen detection, and genotyping. Recently, this technique has been used to develop molecular markers and to evaluate critical aspects for olive oil authentication (Giménez et al. 2010).

This study used RT-PCR as a tool in the marker-assisted selection (MAS) in crop plants in general, and wheat in particular. Screening for stem rust resistance gene *Sr24* by RT-PCR was carried out using primers specific to a SCAR marker.

Materials and methods.

Plant material. The wheat genotypes and segregating lines used in this study are listed in Table 1.

DNA extraction and quantification. DNA was extracted from the leaves of 1 month old wheat seedlings according to Nalini et al. (2004). The DNA was quantified by using fluorimeter (Hoefer DyNA Quant 200).

Polymerase chain reaction. PCR screening used a Realplex4 (Eppondorf, Germany). A SCAR marker (SCS1302609) for the *Sr24*/*Lr24* gene (Gupta et al. 2006) using specific primers (5' CGCAGGTTCCAAATACTTTTC 3' and 5' CGCAGGTTCTACTAATGCAA) were used in a total volume of 25 µl reaction mixture containing 1X PCR buffer (10 mM Tris-HCl (pH-9.0), 1.5 mM $MgCl_2$, 50 mM KCl, and 0.01% gelatin), 100 µM of each dNTP (Sigma, St. Louis, MO, USA), 0.75 U Taq DNA Polymerase (Bangalore Genei Pvt. Ltd, Bangalore, India), 4.0 picomoles of each primer, 0.4X SYBR green dye (Sigma, St. Louis, MO, USA), and 100 ng of genomic DNA. Amplifications were performed using the following thermal cycling profile: 1 cycle of 94°C for 2 min, 35 cycles of 94°C for 1 min, 60°C for 1 min, 72°C for 1 min, and a final extension of 72°C for 7 min.

Table 1. Screening of genotypes for presence of stem rust resistance gene Sr24 using RT-PCR. Cultviars with an * are the F_2 of the cross 'Kalyan Sona/Vaishali' (phenotyping of the individuals by rust inoculations were by Das et al. (2006). *Sr24* gene status: RR = homozygous, Rr = heterozygous). Melting curve samples were scored positive if the melting temperature was 83.9°C. +/– assay samples were scored as positive if the peak was above the threshold line.

Cultivar	*Sr24* gene status	Scoring for band based on:		
		Ethidium bromide staining followed by PCR	Melting curve	+/– assay
Unnath Kalyan Sona	+	+	+	+
KS-1	+	+	+	+
KS-3	+	+	+	+
Unnath Sonalika	+	+	+	+
FLW-2	+	+	+	+
Kalyan Sona	–	–	–	–
PBW343	–	–	–	–
MACS 2496	–	–	–	–
B-6 (154A)	+	+	+	+
Vaishali	+	+	+	+
Vidisha	+	+	+	+
Agra Local	–	–	–	–
163B*	+ (RR)	+	+	+
163C*	+ (Rr)	+	+	+
164A*	+ (RR)	+	+	+
164B*	+ (Rr)	+	+	+

Analysis of results. The presence or absence of a band in MAS were analyzed in three ways, using a quantification curve, by a melting analysis, and using a +/– assay of the RT–PCR technique. To compare RT–PCR results, PCR products were resolved on 2% agarose gels, stained with ethidium bromide solution (0.5%), and visualized under a UV transilluminator where the presence or absence of bands were scored.

Results and discussion. The protocol parameters were optimized. We observed that samples with DNA concentration of 100 ng and a primer concentration of 4.0 picomoles (each) gave well resolved peaks. Thermal cycling conditions were similar to that used in the Master Cycle Gradient 5300.

Analysis using a quantification curve. Progress of DNA amplification during PCR could be monitored in real time by measuring the intensity of fluorescent dyes during amplification using quantification curve. A quantification curve is the curve obtained by plotting the increase in fluorescence (Y axis) as the amplification of the target DNA is started (X axis). Carriers increase in fluorescence as the amplification of target DNA started, and noncarriers of *Sr24* gene showed no increase in fluorescence because it lacks the target DNA (Fig. 1). However, using a quantification curve for the analysis needs to be further standardized.

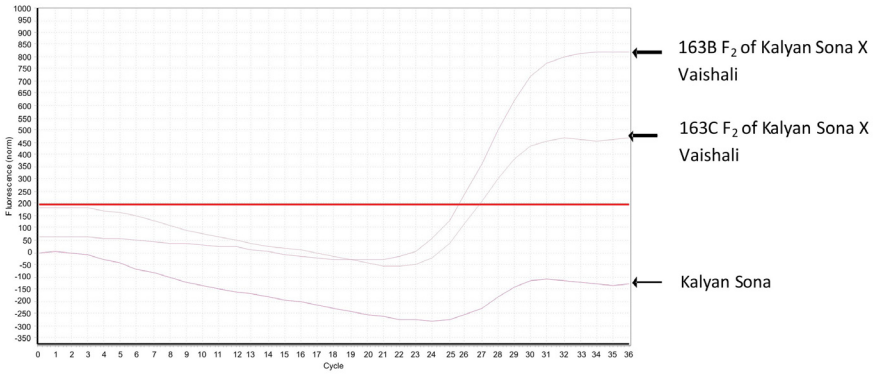

Fig. 1. Analysis of results based on a quantification curve. Carriers of the *Sr24* gene, such as 163B and 163C, show sharp peaks above the threshold level of 200 fluorescence units, whereas the noncarrier Kalyan Sona does not show any peak.

Analysis using a melting curve. Melting curves were performed at the end of SYBR green quantitative RT–PCR to check for primer-dimer or nonspecific product formation. Using plots of dI/dT against temperature after amplification, the results were analyzed using peaks indicating the Tm (melting temperature) of the amplified products. From the melting curve analysis, we could differentiate between individuals carrying *Sr24* gene and noncarriers (Table 1, p. 21). We also could distinguish homozygous *Sr24* (RR) individuals from heterozygous individuals (Rr) (F_2 of 'Kalyan sona / Vaishali) and also the susceptible parent (rr). The peak height of a heterozygous plant was approximately half that of a homozygous plant (Fig. 2).

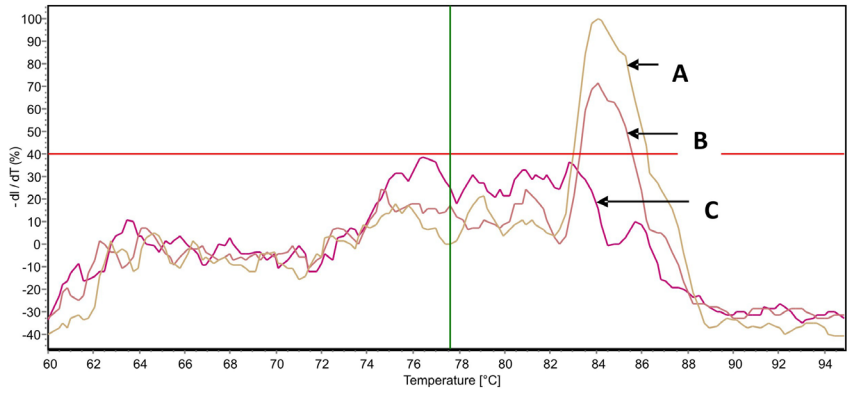

Fig. 2. Analysis of results based on a melting curve. The melting temperature was approximately 83.9°C. A – relative fluorescence units was 120% for carriers of the *Sr24* gene with homozygous allele 163B*; B – 163C* with heterozygous allele for *Sr24*, the relative fluorescence unit was 70%, approximately half that of homozygous 163B; and C – Kalyan Sona with no peak. * F_2 'Kalyan Sona (susceptible parent, rr) / Vaishali (*Sr24*).

Analysis by +/– assay. In RT–PCR, the +/– assay can be used to score the presence or absence of a marker/gene based on the quantification curve, where an increase in the fluorescence unit above a threshold level will be considered positive and below the threshold level will be considered negative. The threshold level also can be manually adjusted and examined for positives and negatives of the *Sr24* gene (Table 1, p. 21).

Conclusions. In MAS, a large number of populations have to be screened using conventional PCR techniques, and requires post-PCR processing, such as resolving in agarose gels, which is time consuming and sometimes may lead to false results due to cross contamination. To overcome these delays and errors, and also to screen a large number of populations, the RT–PCR technique has been used to screen a large number of samples for the presence or absence of a gene of using specific primers. Application of RT–PCR in MAS has not been reported in literature, but the use of this technique for the development of molecular markers has been reported in olive plants by Giménez et al. (2010). We used a specific primer for a SCAR marker reported for stem rust resistance gene *Sr24* (Gupta et al. 2006). The results of phenotypic

and genotypic data of conventional PCR and RT–PCR (melting curve) were compared, and they were found to match exactly, indicating the advantage of using RT–PCR in MAS. This method could avoid post-PCR processing with agarose gel electrophoresis and, thereby, save time. However, the use of a quantification curve for the analysis needs further standardization.

Acknowledgements. The authors would like to thank Dr. S.F.D'Souza, Head, NABTD and Dr. S.K. Apte, Head, MBD, for their constant encouragement and support. A part of the work was carried out by Ms. Kiruba Shankari (Project Trainee) at BARC.

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Threshability in recombinant inbred lines of wheat.

S.G. Bhagwat.

Recombinant inbred lines of bread wheat arising from two cultivars. Kalyan Sona and Sonalika. were raised in the field at Trombay in 2010–11 season. The lines were sown at two sowing dates corresponding to normal and late sowing. At harvest, one spike each from each RIL was collected at random. Spikelet number and rachis length were recorded. The spikes were threshed by hand and a rating was given, beginning with 1.0 for the softest threshing up to 5.0 for very hard threshing.

Results and discussion. As in earlier years, Kalyan Sona was softer threshing than Sonalika. The RILs showed differences in threshability. Lines softer and harder than the parents were observed. The distribution for threshability of the late sown lines is shown in Table 2. Correlation coefficients were calculated between some of the traits using Microsoft Excel (Table 3).

A significant correlation was found between the threshability ratings for 2009–10 and 2010–11. Although the ratings are based on single spikes and are recorded using a subjective assessment, the correlation showed that the procedure gave repeatable results. Lower ratings were less consistent and the reliability was better for lines with higher ratings. When the ratings were for soft (1.0 to 2.5), intermediate (3.0 and 3.5), and hard (4.0 to 5.0), the frequencies were 52, 62, and 24 (2009–10) and 68, 46, and 24 (2010–11), respectively. Significant correlations for rachis length and spikelets/cm of rachis indicated that the RILs were stabilized for these traits. These RILs could be used to identify loci governing threshability and spike morphology.

Table 2. Scores for threshability in field grown recombinant inbred lines between Kalyan Sona (soft threshing) and Sonalika (hard threshing). Spikes were rated from 1.0 for the softest threshing up to 5.0 for very hard threshing.

Description	Rating	Frequency
Very soft	1.0	17
Intermediate	1.5	00
Kalyan Sona type	2.0	45
Intermediate	2.5	06
Sonalika type	3.0	25
Intermediate	3.5	21
Hard threshing	4.0	15
Intermediate	4.5	02
Very hard threshing	5.0	07

Table 3. Correlation coefficients between selected traits for "Kalyan Sona/ Sonalike' recombinant inbred lines (RIL). ** indicates significance at the 1% level.

Trait	Number of RILs	Correlation coefficient
Threshability rating; 2009–10 and 2010–11	138	r = 0.56**
Rachis length; 2009–10 and 2010–11	130	r = 0.54**
Spikelets/cm of rachis; 2009–10 and 2010–11	137	r = 0.58**

During the domestication of bread wheat, selection for the free threshing habit enhanced its suitability for cultivation. Two mutations, *q* to *Q* on chromosome 5A and *Tg* to *tg* on chromosome 2D, mainly are responsible for the free threshing habit of bread wheat. Because threshability is an important trait, many studies have sought to map the loci involved. Jantasuriyarat et al. (2004) analyzed the ITMI mapping population and observed that two QTL that affected threshability were located on chromosomes 2D and 5A. The QTL on 2D probably represented the effect of *Tg*, the gene for tenacious glumes. The QTL on 5A are believed to represent the effect of *Q*. Free threshing-related characteristics were more affected by *Tg* and to a lesser extent by *Q*. Other QTL that were significantly associated with threshability in at least one environment were located on chromosomes 2A, 2B, 6A, 6D, and 7B.

Nalam et al. (2007) analyzed RILs developed by ITMI and a 'Chinese Spring/Chinese Spring 2D' F_2 population and observed that in the ITMI population, two QTL affected threshability and their location coincided with the two QTL affecting glume tenacity. In the 'Chinese Spring/Chinese Spring 2D' F_2 population, the location of QTL that affected glume tenacity coincided with *Tg1*. These results suggest that the effect of *Tg1* and threshability is through the level of attachment of the glumes to the rachilla. In our experiments, we observed that RILs obtained from two free-threshing cultivars showed variation for threshability. The variation was studied using hand threshing. More observations were made during the winter season of 2010–11, which are reported here.

Acknowledgement. To Shri Vikas and Shri Sudhakar Mali for help with the field work.

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Current activities.

Suman Bakshi, S.G. Bhagwat, Chun Mei Chang, and A.S. Shitre.

Bread wheat cultivars were grown in a replicated experiment and measurements were made on the canopy temperature depression. Another study monitored translocation of reserves from stem to the grain. Analysis of the data is in progress. An RIL population from the intervarietal cross 'Sonalika/Kalyan Sona', a bread wheat RIL population for grain protein content, and early flowering mutant lines in the background of cultivar C306, genotype MP3054, and Hindi62 were carried forward. Grain size and shape mutants of the long grain durum genotype PBND 1625 and morphological mutants in a bread wheat genotype carrying multiple phenotypic markers were carried forward. The backcross populations carrying sphaerococcum locus in Kalyan Sona background were carried forward. Other genetic stocks, such as an ADH variant (tall and dwarf) and a lax mutant of sphaerococcum type in Kalyan Sona background were carried forward.

Wheat seeds are exposed to soil conditions after sowing, which may include salinity and could affect germination. Seeds of *T. turgidum* subsp. *dicoccum* and *T. aestivum* subsp. *aestivum* were soaked in increasing concentrations (100–500 mM) of NaCl and the germination percent and seedling height were measured. We observed that the germination percent decreased beyond 300 mM; seedling growth was reduced by 40–45% at 100 mM. The aleurone layers of *T. turdigum* subsp. *dicoccum* and *T. aestivum* subsp. *aestivum* were incubated in liquid medium in the presence of different concentrations of NaCl and assayed for amylase stimulation, protein secreted in medium, mitochondrial activity, and weight loss. There was no effect on secreted protein, however, amylase stimulation, respiration, and weight loss were affected by NaCl.

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Performance of timely and late-sown cultivars under different sowing times.

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Summary. A field experiment was conducted during winter seasons of 2005–06 to 2006–07 at the Directorate of Wheat Research, Karnal, to evaluate the timely sown and late sown recommended cultivars under normal, late, and very late sowing conditions. A clear picture will be provided as to whether or not timely sown cultivars perform equally good under late and very late sowing conditions. A pooled analysis of two years data revealed a reduction grain yield of 14.4% as sowing was delayed from normal to late sown conditions. Cultivar differences were observed for anthesis, maturity, spike length, grain-filling period, grain production rate, and yield and yield attributing parameters. The interaction between sowing time and cultivars was significant for grain yield. Three timely sown cultivars (PBW 343, HD 2687, and PBW 502) performed better under normal sowing condition whereas the late-sown cultivar UP 2425 produced a maximum grain yield (42.24 q/ha) under late sowing conditions and Raj 3765 produced a maximum grain yield (42.79 q/ha) under very late sowing conditions, which was significantly higher than other cultivars. The resultsshowed that timely sown cultivars did not perform better across the sowing time and that there is a need to develop different cultivars for various sowing conditions.

Introduction. Wheat is the second most important crop after rice in India and in 2008–09 occupied approximately 28×10^6 ha with a production of 78.4×10^6 metric tons. India ranks second in wheat production after China. The area, productivity, and production of wheat have increased 119, 236, and 634%, respectively, since 2005 compared with 1965–66 (base year). Weather is cool and dry in the early part of wheat-growing season (November to February) whereas temperature rises during the grain-filling period (March–April), which is more pronounced in eastern part of Indo-Gangetic plain, resulting in a reduced wheat-growing period. Wheat is grown under different agroclimatic conditions each having variable productivity levels. In India, wheat is generally grown under three sowing conditions, i.e., normal (November sown), late (December sown), and very late sown (January sown) conditions. The normal sown wheat crop is generally preceded by crops such as upland rice, soybean, sorghum, bajra, or even grown after fallow. The late sown wheat crop is generally preceded by crops such as basmati rice, low land rice, cotton, and pigeon pea and very late-sown wheat is grown after toria, pea, potato, and sugarcane ratoon. Delayed wheat sowing (normal to late, mid-November to the first two weeks of December) resulted in a decrease in yield by 15.5, 32.0, 27.6, 32.9, and 26.8 kg/ha/day under NHZ, NWPZ, NEPZ, CZ, and PZ, respectively, for the timely sown cultivars. For the late-sown cultivars, a delay in sowing (late to very late, first two weeks of December to the first two weeks of January) decreased the grain yield by 42.7, 44.8,

51.6, and 44.2 kg/ha/day under NWPZ, NEPZ, CZ, and PZ, respectively (Tripathi et al. 2005).

Some of the scientists think that timely sown recommended varieties do equally well under late and very late sown conditions even under Indian subcontinent where hot and dry wind prevails during the grain-filling period. If this holds true, then the separate breeding programs for late sown conditions are not neede. To test this hypothesis, we selected a set of timely sown and late sown recommended cultivars and grew them under normal, late, and very late sown conditions.

Materials and methods. A field experiment was conducted during the 2005–06 and 2006–07 winter seasons at the Directorate of Wheat Research, Karnal (Latitude 290 43' N, longitude 760 58' E and altitude 245 m). Six culivars, three timely (PBW 343, HD 2687, and PBW 502) and three late sown (PBW 373, UP 2425, and Raj 3765), were evaluated under normal, late, and very late sown conditions. The experiment was conducted in split-plot design and replicated three times. Three sowing times in main plot, i.e., normal (11 and 12th November in 2005 and 2006), late sown (9th and 12 th December in 2005 and 2006), and very late sown (5th and 6th January in 2006 and 2007). After harvesting rice as a fore crop, the field was prepared with a cultivator and disk and in each subplot 250 viable seeds were planted. Fertilizer (150 N, 60 P_2O_5, 40 K_2O) was applied to the crop. A one-third dose of nitrogen in the form of urea, full phosphorous in the form of diammonium phosphate, and potash in the from of muriate of potash was applied as basal, i.e., before sowing and the remaining nitrogen was top dressed in two splits at the first node stage (DC 31) (Zadoks et al. 1974) and at boot stage (DC 41). Irrigation was applied as needed. Weeds were controlled with an application of sulfosulfuron 25 g/ha in 400 liters of water 30 days after sowing. Observations were recorded on biomass, anthesis, maturity, grain-filling period, and grain-production rate, yield and its component characters. Standard statistical methods of analysis were followed for the parameters under study (Gomez and Gomez 1984).

Results and discussion. Delayed sowing from normal to late and very late increased the canopy temperature depression significantly, whereas other parameters such as anthesis, maturity, spike length, and grain-filling period were reduced as sowing was delayed. The difference between the time taken for anthesis under normal and very late sown situations was about 25 days, whereas for grain-filling period, the difference was only 5 days. Canopy temperature depression under very late sown conditions was almost double that of the timely sown plants, whereas spike length was reduced about 1.5 cm when very late sown. Yield and yield-attributing parameters also were significantly different due to sowing time in both the years. From mean of two years, grain yield was reduced to 14.4 % as sowing was delayed from normal to late sown conditions. This observation is in agreement with findings of Tripathi et al. (2005). Protein content increased in delayed sowing.

Cultivar differences were observed for anthesis, maturity, spike length, grain-filling period, grain production rate, and yield and yield-attributing parameters (Table 1 and Table 2, p. 27). PBW 343 took 90 days for anthesis,

Table 1. Effect of sowing time and cultivar on anthesis, maturity, canopy temperature depression (CTD), spike length, grain-filling period, and grain production rate.

Treatment	Canopy temperature depression		Anthesis (days)		Maturity (days)		Spike length (cm)		Grain-filling period (days)		Grain production rate (kg/ha/day)	
Sowing time	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**
Normal	1.98	1.93	101	100	134	134	8.7	8.5	33	34	130	141
Late	2.13	2.07	88	90	119	119	7.6	7.5	31	30	136	122
Very late	4.29	3.86	76	78	106	106	7.2	7.0	30	28	130	140
C D at 5 %	0.38	0.42	0.1	0.6	0.9	0.9	0.2	0.3	0.8	0.3	8.5	11.6
Cultivar												
PBW 343	2.80	2.62	91	90	122	121	7.3	7.0	31	31	136	134
HD 2687	2.86	2.64	89	90	121	119	7.9	7.7	31	29	130	142
PBW 502	2.96	2.63	90	90	121	121	7.4	7.2	30	31	143	132
PBW 373	2.79	2.76	89	89	121	121	7.0	6.8	32	32	134	131
UP 2425	2.71	2.52	86	89	116	119	8.9	8.9	30	30	136	129
Raj 3765	2.70	2.56	84	87	118	119	8.5	8.3	34	31	115	138
CD at 5 %	NS	NS	0.1	0.6	0.3	1.0	0.5	0.4	0.3	1.0	5.5	10.7

Table 2. Effect of sowing time and cultivar on yield, yield-attributing parameters, and protein content.

Treatment	Spikes/m²		1,000-kernel weight (g)		Grains/spike		Yield (q/ha)		Biomass (q/ha)		Protein (%)	
Sowing time	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**	**05–06**	**06–07**
Normal	339	337	41.22	45.15	32.2	32.7	43.32	48.29	109.12	111.72	9.55	11.00
Late	393	389	40.89	32.07	26.5	30.0	42.15	36.25	108.79	88.81	9.01	11.58
Very late	335	330	35.89	39.79	33.3	31.2	39.17	39.54	100.59	80.81	11.03	11.53
C D at 5 %	48	39	0.91	2.39	5.11	4.8	1.87	3.76	7.99	7.16	1.13	0.54
Cultivar												
PBW 343	352	349	38.67	36.95	31.6	33.9	42.12	42.22	100.86	95.21	9.83	11.32
HD 2687	342	339	37.00	35.26	33.1	34.8	40.56	41.61	107.67	101.39	8.95	11.07
PBW 502	368	362	40.89	40.72	29.2	28.9	42.87	40.59	105.09	99.38	10.08	11.41
PBW 373	374	376	39.22	43.77	29.7	26.3	43.21	42.09	106.61	101.54	10.16	11.51
UP 2425	335	331	39.00	39.43	32.3	30.9	40.72	39.12	110.32	91.97	10.15	11.58
Raj 3765	361	355	41.22	37.89	28.1	32.6	39.79	42.51	106.48	89.19	9.97	11.53
CD at 5 %	32	32	1.23	5.50	3.1	5.5	1.84	3.05	4.69	8.11	1.27	0.45

whereas the late sown cultivar Raj 3765 was 86 days. All cutivars matured in 119 to 121 days. Late sown cultivar UP 2425 possessed longest spike length, which was significantly higher than others. The greatest number of spikes/m² was observed in PBW 373 and the lowest in UP 2425. Thousand-kernel weight was greatest in PBW 502 and the lowest in HD 2687. PBW 373 produced the maximum grain yield (42.65 q/ha) followed by PBW 343 (42.17 q/ha); the minimum was in UP 2425 (39.92 q/ha).

A significant interaction between sowing time and cultivar was observed for grain yield. All the three timely sown cultivars (PBW 343, HD 2687, and PBW 502) performed better under timely sown conditions, whereas late sown cultivar UP 2425 produced the maximum grain yield (42.24 q/ha) under late sown conditions, which was significantly higher than yield obtained by timely sown cultivars HD 2687 and PBW 502 under late sown conditions. Under very late sown conditions, Raj 3765 produced the maximum grain yield (42.79 q/ha), which was significantly higher than other cultivars (Table 3). Thus, the hypothesis that timely sown cultivars will perform better under late and very late sown conditions was not true. The few late sown cultivars that exceeded the yield level over timely sown cultivars under late and very late sown situations provides a sound reason for developing cultivars separately for timely sown and for late sown conditions.

Table 3. Interaction between sowing time and cultivar on grain yield (q/ha, pooled basis). TS = timely sown recommended cultivar and LS = late sown recommended cultivar.

	Sowing time			
Cultivar	**Normal**	**Late**	**Very late**	**Mean**
PBW 343 (TS)	47.97	40.66	37.88	42.17
HD 2687 (TS)	47.68	36.73	38.86	41.09
PBW 502 (TS)	47.85	38.89	38.46	41.74
PBW 373 (LS)	47.09	42.24	38.63	42.65
UP 2425 (LS)	43.48	36.78	39.50	39.92
Raj 3765 (LS)	40.76	39.91	42.79	41.15
Mean	45.80	39.20	39.35	
CD at 5 % (sowing time)			2.00	
CD at 5 % (cultivar)			1.58	
CD at 5 % (sowing time x cultivar)			3.18	

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Pathogenic evolution of wheat rust pathogens in relation to resistance genes in Indian wheat cultivars – some suggestions for strengthening wheat rust resistance in India.

Wheat (*T. aestivum*, *T. turgidum* subsps. *durum* and *dicoccum*) is one of the prime cereal crops of India and is attacked by the three rusts, stem or black, leaf or brown rust, and stripe or yellow rust. Stem rust survives throughout the year only in the Nilgiri Hills of southern India. The Himalayas in northern India are too cold for the pathogen to survive during winter. Therefore, after the wheat harvest in the Nilgiris Hills of southern India, stem rust drastically disappears from India because of low inoculum build up in absence of the host. A *P. striiformis* that needs low temperature survives for the whole year in the Himalayas is of epidemic consequences to the wheat crop in Himachal Pradesh, Uttranchal, Punjab, Haryana, West Uttar Pradesh, and north Rajasthan. Leaf rust needs an intermediate temperature, and, thus, survives and spreads from both southern and northern foci and is important throughout India (Nagarajan and Joshi 1985). Systematic work on wheat rusts in India began in 1931 by Dr. K.C. Mehta. We haver made an effort to update the list of rust races that have prevailed in different parts of India since 1975 by consulting ICAR monographs (Mehta 1940, 1952) and Annual Wheat Workshop Reports regularly released by the All India Coordinated Wheat and Barley Project, previously from the IARI, New Delhi, but now from the Directorate of Wheat Research (ICAR), Karnal (Table 1).

Table 1. New pathotypes in Indian rust flora over the years. New race names are based upon the binomial system of nomenclature of Nayar et al. (1997, 2003).

Period	Stem/black rust	Leaf/brown rust	Stripe/yellow rust
Up to 1975	11, 11A, 14, 15, 17, 21, 24, 24A, 34, 34-1, 40, 42	10, 11, 12, 12a, 17, 20, 63, 77, 106, 107, 108, 162	13, 14, 19, 20, 31, 38
1975–80	21-1, 40A, 21A-2	77A, 104	14A, 20A, 38A, I
1980–85	117A-1	114A, 104B, 12-2	K
1985–90	40-1,117-1	77-1, 77-2, 77-3, 12-1, 12-3, 12-4, 107-1, 108-1	L, N, P
1990–95	117-2, 117-3, 117-4, 117-5, 117-6	77-4, 77-5, 104-2, 104-3	T, U, CI, CII, CIII
1995–2011	40-2	77-6, 77-7, 77-8, 77-9, 77-10	*Yr9* virulence (46S119 and 78S84)

Changes in the distribution patterns of wheat rust pathotypes in India – an historical account.

Vast areas under high-yielding wheat cultivars resulted in changes in the frequency and spectrum of stem, leaf, and stripe rust pathogens. Race 12 (5R5) of *P. triticina* was the most predominant between 1972 and 1977 in the north and east zones with an overall frequency of 46%. During this period in the Nilgiris Hills in southern India, race 77 (45R31) was predominant with a frequency as high as 56%. Race 12 (5R5), although it virulence for very few genes, remained most predominant in the country during these five years, except in the Nilgiris Hills. Race 104 (17R23), which was first detected in samples from Nepal in 1972, was the second most prevalent race and predominated between 1972–77. However, the frequency of these races declined during 1982–87 and were replaced by 104B (29R23). Although the frequency of race 77 (45R31) declined in the Nilgiris Hills to 5% in 1982–87, it became most predominant race in the Northern Hills, Northern Plains, and Eastern and Far Eastern zones replacing the virulent race 12 (5R5). The increase in the frequency of race 77 (45R31) in rest of India appears primarily due to the increase in area of cultivars specifically susceptible to race 77. A second reason may be the presence of a greater number of virulence genes. In the Nilgiri Hills, other biotypes of race 77, possessing additional pathogenicity for *Lr10* and *Lr10+Lr26*, replaced race 77 (45R31). This group of biotypes is well distributed all over India and was found in over 46% of the samples analyzed. The shift in virulence pattern from races 12 (5R5), 104 (17R23), and 77 (45R31) in 1972–77 to 77A (109R31), 77A-1 (109R23), 77-1 (109R63), and 104B (29R23) in 1982–87 is the result of a shift in varietal pattern over different parts of India (Table 2, p. 29). *Puccinia striiformis* races 14(66S0), 20 (70S0) and 38 (66S0-1) prevailed in India before the cultivation of dwarf wheats. After widespread cultivation of Mexican wheats, three variants 14A (66S64), 20A (70S64), and 38A (66S64-1) predominated during 1975–80 in northwest India. Race I (38S102), which matches Sonalika, predominates in

the Nilgiri Hills. Since 1982, race K (47S102) had the highest frequency in northwest India until the emergence of new races N (46S102), P (47S103), and *Yr9* (46S119 and 78S84) (Table 3).

Table 2. Population shift in *Puccinia triticina* over the years and consequential breakdown of erstwhile cultivars/ genes.

Period	Prevalent population (>60% frequency)	Important new races emerged/ built up	Susceptible genes/genotypes
1961–65	20, 77, 162	107A, 162A, 17, 131	NP770 and NP824, NP710 and NP809, *T. turgidum* subsp. *dicoccum*
1966–70	12, 77, 162, 162A	104, 104A, 77A	*Lr3*: Democrat, Bowie, Texas *Lr10*: Federation, Gabo, Ridley
1971–75	12, 77, 104A, 162	104B	Sujata, C306, Sonora 64 *Lr13*: Sonalika, Kalayansona, Lerma Rojo
1976–80	12, 77, 104B	77A-1	*Lr13*: HD2009, WL711
1981–90	104B, 77A-1	12-3, 77-3, 77-4, 107-1, 108-1	*Lr23*: HD2285, HI977, DL153-2, GW173, HD2278, K8804 *Lr10+Lr13*: HD2329
1991–97	77-3, 77A-1	77-5, 104-2, 104-3	*Lr26*: WH3004, UP2338, CPAN3004, DWR162, HP42, HS277
1997–2011	77-5	77-7, 77-8, 77-10	*Lr9* by 77-7, *Lr19* by 77-8 and *Lr28* by 77-10

Table 3. Population shift in *Puccinia striiformis tritici* over the years and consequential breakdown of erstwhile cultivars/genes.

Period	Prevalent population (>60% frequency)	Important new races emerged/ built up	Susceptible genes/genotypes
1961–65	14, 19, 20, 31, A	38	NP770, 792, 809, 824, 710, NP200, 201, 202, K65, C591
1966–75	14, 19, 20, 38, A	14A, 20A, 38A	*Yr2*: Kalyansona, Sonalika, Lerma Rojo, Sonora 64
1976–85	20, 38, 14A	I, K	*Yr2* (KS): WL711, Kalyansona, HD2009
1986–90	12, 77, 104B	77A-1	*Lr13*: HD2009, WL711
1991–96	N, K	P, race *Yr9*	*Yr9*: WH542, CPAN3004, UP2338
1997–2011	*Yr9* virulences	—	*Yr9*: PBW 343, DBW 17

New variability in rust pathogens renders genes ineffective from time to time.

The wide-spread cultivation of high-yielding cultivars over a large area with a high level of disease resistance since 1970 exerted directional selection pressure on the rust pathogen population. In response, new rust pathogens evolved to match the resistance genes incorporated into the new wheat cultivars. In *P. triticia*, 17 new races emerged after 1970 from different regions of the country. The additional virulence was observed in race 12 (5R5) for *Lr20+Lr23*, *Lr23*, *Lr26*, *Lr15+Lr26*, *Lr9*, *Lr19*, and *Lr28*. The race 104 (17R23), isolated from Nepalese samples in 1972, has now arisen with biotypes having virulence for *Lr20*, *Lr23*, and race 77 (45R31) has acquired virulence to *Lr10*, *Lr10+Lr23*, and *Lr10+Lr26*.

For *P. striiformis*, eight new races or biotypes were encountered over the last 20 years; 14A (66S64), 20A (70S64), and 38A(66S64-1), all virulent on Kalyansona; I (38S102), which matched Sonalika and Strubes Dickopf; and *Yr1*, L (70S69), N (46S102), L (70S69), and P (47S103) had additional virulence for hybrid 46 (*Yr3b*, *Yr4b*), Chinese 166 (*Yr1*) and *Yr3a+Yr4a*. *Yr9* races have now emerged and spread into the northwest plains, where a major portion of the area is under cultivation with wheats having the *Yr9* gene.

For *P. graminis tritici*, the evolution of new races has been comparatively less, because wheat cultivation is not that intensive in the Nilgiri Hills of southern India (inoculum source for stem rust target areas). The most remarkable emergence of a new race has been that of 40-1, which is virulent on gene *Sr24* and present in very few cultivars released for cultivation in southern, central, and peninsular India.

Rust-resistant stocks used in Indian wheat breeding programs for protection from leaf and stripe rusts.

The 'boom and bust' cycle, which occured particularly after the introduction of Mexican semidwarf wheats in the Indian subcontinent, was eliminated by incorporating effective rust resistance genes (*Lr* and *Yr*) using specific resistant donor lines in Indian wheat breeding programs (Tables 4 and 5).

Table 4. *Lr* genes used to date in Indian wheat breeding programs for leaf or brown rust resistance.

Gene	Source	# of cultivars/lines	Cultivar/line name
Lr1	Malakoff, Sharbati, Sonora	4	Khushal 69, Moti, UP301, MP846
Lr3	Democrat (CI 3384)	1	CPAN1235
Lr10	Lee, Timstein	6	BW11, NI747-19, I5439, HD2009, HD2329, HS86
Lr11	Hussar (CI 4843)	1	HS86
Lr13 APR	Thatcher, Frontana	7	UP115, WL2265, PBW65, HS86, IWP72, Sonalika
Lr14	Hope, H44	2	Sonalika, WL711
Lr17	RL6041, 6008	1	NP846
Lr23	Gaza durum	13	HI977, HYB65, HD2135, HD2270, HD2278, HD2204, HD2258, HD2281, HD2285, HUW213, UP262, DL153-2, Girija
Lr26	*Secale cereale*	22	HUW206, AKW1071, CPAN1874, DL802-3, DL803-2, CPAN1922, CPAN3004, DWR162, DWR195, GW190, HD2610, HPW42, HS207, HS240, HS277, HUW318, K8804, MACS2496, PBW299, 343, UP2338, WH542
Lr34	Chinese Spring	23	C306, DWR39, GW173, HD2189, HD2329, HD2501, 2610, HI977, 1077, HP1209, HPW42, HS207, 240, 295, K9006, Kalyansona, NI5439, PBW175, PBW299, UP262, UP2338, WH147, WH54

Table 5. *Yr* genes used to date in Indian wheat breeding programs for resistance to stripe or yellow rust.

Gene	Source	Documented line
Yr2	Heines VII type	HD2009, 2189, 2278, 2285, 2329, 2380, HI977, 1077, HP1209, 1633, HS86, HUW234, HW741, HW971, IWP72, J405, K8020, NI5439, PBW175, PBW222, RAJ2184, RAJ3077, Sonalika, Swati, UP262, VL421, VL616, WH283
Yr2 (KS)	Heines VII type B	W11, GW173, HD2402, HD2428, HDR77, HI1123, HP1102, HUW234, K7410, K8027, LOK-1, PBW65, WL711
Yr3	Vilmorin type	HS295
Yr9	*Secale cereale*	CPAN1922, 3004, DL803-3. WR162, 95, GW190, HD2610, PW42, HS207, 240, 277, HUW206, 318, K8804, MACS2496, PBW299, 343, UP2338, WH533, 542
Yr18	*Lr34* sources	C306, DWR39, GW173, HD21892, HD2329, HD2610, HI1077, HP1209, HPW42, HS207, 295, K8962, K9006, NI5439, PBW175, 299, UP2338, WH147, 542

In search of additional/new genes.

Unfortunately, the genetic base of rust resistance in India wheat cultivars languishes in front of the array of new pathotypes that have emerged or built up during the last 2 to 3 decades. To sustain wheat yields in India, the search for new genetic sources of resistance becomes imperative. A number of genes are available and need to be exploited to alleviate resistance base of Indian wheat germ plasm (Tables 6 and 7).

Table 6. Unutilized genes for resistance to leaf or brown rust useful for Indian wheat breeding programs.

Gene	Source	Remarks
Lr2a	Webster (CI 3780)	Useful component of multiple gene resistance.
Lr4–Lr8	Waban (CI 12992)	Difficult to characterize, not of much use.
Lr9	*Ae. umbellulata*	Present in very limited Indian cultivars, widespread effectiveness.
Lr11	Hussar (CI 4843)	Temperature insensitive, slow ruster.
Lr12	Spring	Adult-plant resistance.
Lr15	Kenya W1483	Temperature sensitive, effective at 15–18°C.
Lr16	Selkirk	Frequency of virulence remains low.
Lr17	Timson	Useful in multiple gene resistance.
Lr18	*T. timopheevii*	Temperature adability.
Lr20	Thew, Chinese Spring	Durable resistance
Lr21	*Ae. tauschii* var. *meyeri*	Adult-plant resistance.
Lr22	*Ae. tauschii*	No known virulence.
Lr24	*Thinopyrum ponticum*	Undesirable red grains.
Lr25	*Secale cereale* cv. Rosen	No known virulence.
Lr27+Lr31	CS*6/Hope 3B	Complementary genes.
Lr28	*Ae. speltoides*	No virulence in India.
Lr29	*Th. ponticum*	Virulence in Pakistan and Turkey.
Lr30	Terenzio	Slow ruster.
Lr32	*Ae. tauschii* (RL 5497-1)	Wider stability.
Lr33	Thatcher*6/PI 58548	Effective in combination.
Lr35	*Ae. speltoides*	Adult-plant resistance.
Lr36	*Ae. speltoides*	Not studied much.
Lr37	*Ae. ventricosa*	Effective field resistance.
Lr38	*Th. intermedium*	Virulence unknown.
Lr39–Lr44	*Ae. tauschii*	Not studied much.

Table 7. Unutilized genes for resistance to stripe or yellow rust useful for Indian wheat breeding programs.

Gene	Source	Remarks
Yr1	Chinese 166	Becomes susceptible to barley races, world wide.
Yr4	Hybrid 46	Low level of virulence in India.
Yr5	*T. aestivum* subsp. *spelta album*	Rare virulence.
Yr6	Heines Kolben	Higher resistance at low temperature.
Yr7	Iumillo durum	High frequency of virulence worldwide.
Yr8	Ae. comosa	Resistance is not durable.
Yr10	Moro (PI 178383)	No known virulence in India.
Yr11	Joss cambier	Adult-plant resistance (presumed).
Yr12	Mega	Adult-plant resistance (presumed).
Yr13	Maris Huntsman	Adult-plant resistance (presumed).
Yr14	Hobbit	Adult-plant resistance (presumed).
Yr15	*T. turgidum* subsp. *dicoccoides*	Virulence unknown.
Yr16	Cappelle Desprez	Adult-plant resistance and durable resistance.
Yr17	*Ae. ventricosa*	More susceptible at low temperature.
Yr18	Terenzio	Adult-plant resistance.

Durable resistance – global experience and lessons to Indian wheat breeders.

Durable disease resistance remains effective in a cultivar even though it may be widely grown over a long period of time in an environment that favors disease epidemics. This descriptive term does not provide an explanation for the basis of inheritance of this trait. Durable resistance has the following dimensions: 1. covers a large area, 2. grown for many years, and 3. high inoculum load and favorable weather. On the basis of multilocational data on triticale, cultivar Coorong was selected from a CIMMYT trial for widespread cultivation in Australia, because the alien gene *Sr27* gave total resistance to stem rust. Almost immediately after the commercial release of Coorong, stem rust was observed because the pathogen developed matching virulence in Australia. The durability of genotype, therefore, cannot be assessed by means of small field trials or multilocation evaluation for a few seasons. The *Sr26* gene, derived from *Thinopyrum elongatum*, has been used in Australia since 1970, is present in a number of wheats, and is designated as durable. Multilocation tests do not guarantee resistance nor are the alien genes are always durable. Vanderplank rationalized that non-specific or horizontal resistance will neither lead a cultivar into boom-and-bust cycle nor exert any directional selection pressure on the pathogen and, therefore, will be durable. Although Vanderplank considered durable resistance to be a polygenic trait, he cited a number of examples such as the maize–*P. polysora* system in Africa, where a single resistance gene contained the disease for a number of years.

The oat cultivar Red Rustproof is still durable to crown rust even after one-hundred years. The wheat cultivars Thatcher and Lee have withstood stem rust for 55 and 30 years, respectively. Cappelle Desprez has expressed a moderate resistance to stripe rust at the adult-plant stage for the last 20 years. Cappelle Desprez carries both seedling and adult-plant resistance with genes *Yr3a* and *Yr4a*. No detectable race-specific component has been detected in the adult-plant stage in Cappelle Desprez; but all cultivars with *Yr3a* and *Yr4a* have not been durable. Genetic analysis of Cappelle Desprez shows that chromosomes 5BS and 7BS contribute substantially to durable resistance. Further analysis showed that the long arms of homologous chromosomes 5A, 5B, and 5D increase susceptibility, whereas the short arms of these chromosome had the opposite effect. Cappelle Desprez appears to possess an optimal balance between the effects of genetic loci in increasing resistance and those favoring susceptibility.

Several lines derived from H44 and Hope also exhibit durable stem rust resistance. Cultivars such as Thatcher, Lee, Hope, Kenya Page, Africa Mayo, and Selkirk, which have been used globally, possess the *Sr2* adult-plant resistance gene. This gene is tightly linked with the pseudo-black chaff gene and when present in combination with other genes, as in Selkirk, produces a durable resistance. In Australia, wheats with five to six different resistance genes are cultivated. Gene *Sr36* derived from *T. timophevii* (*SrTt-1*) is present in cultivars Mengavi, Mendos, Timson, Cook, Timgalen, and Shortim and in various blends,with *Sr5*, *Sr6*, *Sr7a*, *Sr8*, *Sr9c*, *Sr11*, and *Sr17*. In race surveys, the occurrence of matching virulences was detected for most of the genes either alone or in combination. However, combined virulence for *Sr36* was very low in frequency in Australian wheat despite the fact that *Sr36* was released in varietal background as early as 1967. Therefore, like *Sr2*, combining *Sr36* with other resistance genes can render wheat cultivars durable.

Many host resistance genes that are matched by the pathogen survive in breeding populations for a long time, because these gene are not totally overcome by the pathogen and they still carry some amount of residual resistance. In the barley–*Erysiphe graminis hordei* system, they are referred to as defeated genes. In the wheat–*P. striiformis* system, segregation for resistance to stripe rust can be obtained through minor gene effects, temperature-sensitive genes, adult-plant genes, and various forms of disease resistance. The breeding strategy and selection methodology needs to be viewed accordingly.

Pyramiding resistance genes – one of the effective approaches to curtail fast emergence of new, virulent mutants of rust pathogens.

The idea of pyramiding genes was conceived as an alternative to breeding for polygeneic traits. When only a single resistance gene is present in a host, it soon becomes susceptible. Subsequently, adding one or more resistance genea in that cultivar will increase resistance. Conversely, if four or five cultivars with single resistance genes are grown, all of them are exposed to the same pathogen population and this does not reduce vulnerability to epidemic. However, if these genes are brought into one background, because of additive gene action, the wheat will have resistance to a wide spectrum of pathotypes and the resistance will be durable. Virulence is gained at the cost of fitness, so a pathotype able to infect all the resistance genes in such a cultivar is likely to be less fit in nature and may not induce an epidemic. The approach of pyramiding resistance genes also might prolong their usefulness.

Pyramiding resistance gene provides greater durability if the pathogen is solely dependent on an asexual life cycle and mutation and recombination are less pronounced (Marshall 1977). Combinations of resistance genes have provided good field resistance to wheat stem rust in Australia for several years (McIntosh 1992). Because the alternate host of *P. graminis tritici* is nonfunctional, in Australia pyramiding resistance genes has paid rich dividends. In North America, resistance gene combinations involving *Sr2* have provided durable resistance to stem rust, and *Lr13* and *Lr34* when combined with other leaf rust resistance genes also have provided durable resistance (Kolmer et al. 1991). Pyramiding resistance genes has provided durable resistance in some cases. For instance, the French cultivar Cappelle Desprez has durable resistance to eyespot; the other source is VPM, derived from a cross involving the wild grass *Ae. ventricosa*. Molecular markers linked to these genes have been identified (Worland et al. 1988; Koebner and Martin 1990). Seedlings with both these genes with better eyespot resistance (Doussinault and Douaire 1978) can be selected using molecular markers facilitating selection for better resistance. In view of the rust-management philosophy described above, several unexploited gene(s) may be useful for pyramiding in popular Indian wheat cultivars (Table 8).

Table 8. Suggested sources of adult-plant resistance for strengthening leaf and stripe rust resistance in Indian wheats.

Gene	Source	Remarks
LEAF RUST		
Lr2a	Webster (CI 3780)	Useful component of multiple gene resistance.
Lr11	Hussar (CI 4843)	Temperature insensitive, slow ruster.
Lr12	Spring	Adult-plant resistance.
Lr17	Timson	Useful in multiple gene resistance.
Lr20	Thew, Chinese spring	Durable resistance.
Lr21	*Ae. tauschii* var. *meyeri*	Adult-plant resistance.
Lr22	*Ae. tauschii*	No known virulence.
Lr28	*Ae. speltoides*	No virulence in India.
Lr30	Terenzio	Slow ruster.
Lr32	*Ae. tauschii* (RL 5497-1)	Wider stability.
Lr35	*Ae. speltoides*	Adult-plant resistance.
Lr37	*Ae. ventricosa*	Effective field resistance.
Lr38	*Th. intermedium*	Virulence unknown.
Slow rusters (adult-plant genotypes possessing useful seelding resistance genes in India (Kumar et al. 1999).		
Lr34 alone	HP 1731, C 306	
Lr34+Lr10+Lr13	NIAW 34, HD 2329	
Lr34+Lr23	GW 232, HI 977, HI 1077, GW 173, PBW175	
Lr34+Lr26	PBW 343, PBW 373, HS 240, UP 2363, WH 594, WH 596	
Lr34+Lr23+Lr26	DL 802-3, HS 317, Gabo, Frontana	
STRIPE RUST		
Yr4	Hybrid 46	Low level of virulence in India.
Yr5	*T. aestivum* subsp. *spelta album*	Rare virulence (in snowy conditions only).
Yr10	Moro PI 178383	No known virulence in India.
Yr11	Joss Cambier	Adult-plant resistance.
Yr12	Mega	Adult-plant resistance.
Yr13	Maris Himtsman	Adult-plant resistance.
Yr14	Hobbit	Adult-plant resistance.
Yr15	*T. turgidum* subsp. *dicoccoides*	Virulence unknown.
Yr16	Cappelle Desprez	Adult-plant resistance and proven durable resistance
Yr17	*Ae. ventricosa*	More susceptible at low temperature
Yr18	Terenzio	Adult-plant resistance.

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Genetics of leaf rust and leaf blight resistance in different crosses of common wheat.

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Abstract. Leaf blight caused by *Alternaria triticina* (HLB) and leaf rust caused by *Puccinia triticina* are two of the important diseases of wheat that are widespread in India. Postulating the genes in most of the released cultivars, a chi-square test applied for HLB and leaf rust separately. The HLB reaction in the F_2 generation was a 3:1 (susceptible:resistant) ratio was observed in two crosses, and we conclude that the susceptible reaction is governed by a dominant gene(s) in both the crosses. A 15:1 ratio fitted in three crosses showed that susceptible reaction is governed by duplicate gene(s). Tests also were used for leaf rust reactions to check the validity of expected ratio in the F_2 generation. The 3:1 ratio (susceptible:resistant) fit three crosses and this resistant type reaction is governed by a dominant gene(s). Two crosses fit a 15:1 ratio indicating a resistant type infection governed by duplicate gene(s).

Introduction. Among cereals, wheat is ranked second after rice and is the staple food, especially in northern India, where most people are vegetarian. The crop is grown successfully between an altitude of 30°0–60°0 N and 27°0–40°0 S. Wheat is extensively cultivated under diverse agroclimatic conditions in India covering most of the states except Kerala. All wheat cultivated in India is spring type but grown during the winter. Wheat, the main food crop of India, contributes significantly to the central pool. The cultivation of wheat in India started very early, during prehistoric times and, thus, the origin of wheat is still a matter of speculation. Wheat research to develop high-yielding cultivar and improve management techniques started about a century ago in India. A large number of valuable cultivars were bred and released for commercial cultivation. These cultivars were tall and mainly suited to low-input management with low yield potential. However, a turning point came in the history of wheat breeding during mid-1960s with the introduction of semidwarf, photo-insensitive, high-yielding Mexican wheat breeding material developed at CIMMYT under the guidance of Nobel Laureate Dr. Norman E. Borlaug. These cultivars were tested under the All India Coordinated Wheat Improvement Project and, as a result, three genotypes, Lerma Rojo, S 308, and Sonora 64, which out yielded the old tall wheat cultivars, were released for general cultivation in major wheat-growing areas of India.

Wheat is cultivated on over 217.53 x 10^6 ha in world with 610.87 x 10^6 metric tons produced during 2007–08. The wheat-growing area in India is about 28.00 x 10^6 ha with highest production of 78.4 x 10^6 tons (Anonymous 2008). Globally, the maximum area under wheat is in China followed by U.S.A. and India. In terms of production per unit area, the U.S.A. stands first followed by the Russian Federation. In India, wheat is the main cereal crop and is second only to rice. Uttar Pradesh, Madhya Pradesh, Punjab, Rajasthan, Bihar, Haryana, Maharashtra, and Gujarat are the major wheat-growing states in the country.

Three species of genus *Triticum*, *T. aestivum* subsp. *aestivum* (bread wheat or common wheat), *T. turgidum* subsp. *durum* (macaroni wheat), and *T. turgidum* subsp. *dicoccum* (emmer or khapli wheat) are grown in India. Common wheat, with 2n = 6x = 42 chromosomes, is the most important and mainly grown for chapatti making on a wide area. *Triticum turgidum* subsp. *durum* is grown in some states primarly for pasta products. Stem, leaf, and stripe rust have been major concerns for quite some time, because rust epidemics before or during flowering are most detrimental. The symptoms for stripe rust (also called yellow rust and glume rust) caused by *P. striiformis* usually appear earlier in the spring than symptoms for leaf or stem rust. Leaf rust (also called brown rust) is one of the most common wheat diseases in the world. Rough estimates of up to 40 percent yield losses due to leaf rust at various flag leaf severities and different growth stages have been reported (RL Bowden, personal communication). Leaf rust can inflict serious yield losses in epidemic years (Joshi 1976; Kolomer 1996). Although the disease has more or less been contained in India because of research efforts over the last 50 years, efforts to identify novel genes conferring resistance to this disease need to be continued because of fast evolution of the leaf rust pathogen (Nayer et al. 1996, 2000). So far, nearly 60 genes conferring resistance to leaf rust have been identified and designated *Lr1* through *Lr60* (Mclntosh et al. 2007). Germ plasm collections have been evaluated India for resistance to leaf rust and many accessions the resistance cannot be ascribed to any of the known genes (Shiwani and Saini 1993; Saini et al. 1999). Resistance breeding is the most important control strategy, and its success depends on the identification of resistance genes in genotypes.

Foliar blight is an important disease of wheat occurring all over India, perticularly in major wheat-growing regions and ranks close to rust in destructiveness (Directorate of Wheat Research 1999). The disease occurs as a complex in which causal organisms are *Alternaria triticina* and *Bipolaris sorokiniana*. the disease has been observed from initial stage up to growth stage 47 on Zadoks Scale (Zadok et.al. 1974). The dominant pathogen is *A. triticina* and after growth stage 57, *B. sorokiniana* appears and causes significant damage (Chaurasia et al. 2000). A field heavily infected with *Alternaria* blight diseases presents a burnt look and crop loss may be more than 90 percent (Raut et al. 1983).

Materials and methods. Seven bread wheat cultivars were obtained from Directorate of Wheat Research, Karnal (DBW 14, HUW 468, HUW 533,GW 273, PBW 502, DL 788-2, and PBW 443). The material was grown in a randomized block design with three replications at the Research Farm of Janta Vedic College (JVC), Baraut, Baghpat, during rabi season 2005–06. Each genotype was sown in a 3.0-m three-row plot, keeping the plant-to-plant and row-to-row distance of 10 cm and 23 cm, respectively. All recommended agronomic and cultural practices were adopted to ensure a good crop. A total of five straight cross combinations, I (DBW14/HUW468), II (DL788-2/PBW502), III (DBW14/HUW533), IV (GW273/HUW468), and V (PBW443/HUW533) were attempted and sufficient seed was ensured for each cross. The F_1 generations of all five combinations were advanced at Lahaul and Spiti (HP) during summer 2006. In addition, the BC_1 and BC_2 populations of each combination also were obtained in summer nursery. This way, a complete set of breeding material comprising the seven parents, five each of the F_1, F_2, BC_1, and BC_2 generations was obtained and planted along with an infecter row during the rabi season 2006–07 at JVC. The plot size for the parental lines, F_1s, BC_1, and BC_2 was two 2.5-m rows; each F_2 population was grown in 10 2.5-m rows plot. The entire plot was surrounded by one row with an infector cultivar to create epidemic conditions in the plots.

Result and discussion. ***Leaf blight.*** The inheritance of Helminthosporium leaf blight resistance in bread wheat was studied in five crosses that were screened under artificial epidemic conditions by spraying with a spore suspension of a mixture of virulent races. Plants with less than 46 percent of the leaf area infected were considered resistant and those with a greater leaf area infected were considered susceptible. The F_1s of most all the crosses had a susceptible reaction, indicating dominance of susceptibility over resistance. The chi-square analysis test fit a ratio of 3:1 (3 susceptible:1 resistant) plants in the F_2 generations of crosses I and III, suggesting that the susceptible reaction is governed by dominant gene(s). Plants in the F_2 generation of crosses II, IV, and V segregated 15:1 (15 susceptible:1 resistant), suggesting that susceptibility is governed by duplicate gene in the progenies of these crosses (Table 1, p. 36). These findings are similar to those of Narula et al. (1971) and Kulshrestha et al. (1976) who reported that a susceptible reaction was inherited as a dominant gene in bread wheat. Kaur et al. (2003) reported the susceptible reaction is governed by two dominant genes with complementary effect.

Table 1. Segregation in the F_2 generation of five crosses of bread wheat to foliar leaf blight in the field after artificial inoculation. * Significant at 0.05 % level (X^2 value 3.841 at 1 degree of freedom).

Cross combination	Total plants	F2 reaction						
		Observed		Expected		Expected ration	X^2	Gene action
		S	R	S	R			
DBW14/HUW468	60	49	11	45.00	15.00	3:1	1.422*	Dominant
DL788-2/PBW502	60	56	4	56.25	3.75	15:1	0.017*	Duplicate
DBW14/HUW533	60	48	12	45.00	15.00	3:1	0.800*	Dominant
GW273/HUW468	60	56	4	56.25	3.75	15:1	0.017*	Duplicate
PBW443/HUW533	60	57	5	56.25	3.75	15:1	0.445*	Duplicate

Leaf rust. The inheritance of leaf rust resistance in wheat was studied in five crosses that were screened under artificial epidemic conditions by spraying with an aqueous suspension of urediospores of pathotype 77-5. The parents, F_1s, and F_2 generations also were evaluated for disease severity against pathotype 77-5 at adult-plant stage under field conditions. The leaf rust response and severity was recorded in the F_2. The F_1 plants of all the crosses showed a resistant type reaction, indicating dominance of resistance over susceptibility. The chi-square analysis gave a good fit for a 3:1 (3 resistant:1 susceptible) ratio in the F_2 of crosses II, IV, and V, suggesting that resistance is monogenic dominant (Table 2). A 15:1 (15 resistant:1 susceptible) ratio was found in crosses I and III, indicating that resistance in these crosses is governed by duplicate gene(s). Leaf rust is widespread in India. Most of the released cultivars and advanced varietal trial entries are susceptible to the highly virulent pathotype121R63 (Nayar et al. 2001). These findings agree with those of Nayar et al. (1993, 1997), Datta et al. (2004), Basandrai et al. (2004), Haghparast et al. (2004), and Honrao et al. (2004).

Table 2. Segregation in the F_2 generation of five crosses of bread wheat to leaf rust in the field after artificial inoculation with pathotype 77-5. All F_1 plants had a resistant reaction. * Significant at 0.05 % level (X^2 value 3.841 at 1 degree of freedom).

Cross combination	Total plants	F2 reaction						
		Observed		Expected		Expected ration	X^2	Gene action
		S	R	S	R			
DBW14/HUW468	60	56	04	56.25	3.75	15:1	0.018*	Duplicate
DL788-2/PBW502	60	42	18	45.00	15.00	3:1	0.800*	Dominant
DBW14/HUW533	60	46	14	45.00	15.00	3:1	0.087*	Dominant
GW273/HUW468	60	56	06	56.25	3.75	15.:1	1.440*	Duplicate
PBW443/HUW533	60	51	09	45.00	15.00	3:1	3.200*	Dominant

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ITEMS FROM ITALY

CONSIGLIO PER LA RICERCA E LA SPERIMENTAZIONE IN AGRICOLTURA, Unità di ricerca per la valorizzazione qualitativa dei cereali (CRA–QCE), Via Cassia, 176, 00191 Rome, Italy.

Behavior of wheat cultivars in organic farming tested at the seedling stage with Stagonospora nodorum.

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The Septoria disease complex is caused by two pathogens, *Phaeosphaeria nodorum* (anamorph *Stagonospora nodorum*) and *Mycosphaerella graminicola* (anamorph *Septoria tritici*) that frequently occur together on the same plant in Italy. Both the fungi attack the epigeous parts of the plant with similar symptoms and can cause quantitative and qualitative damage. *Septoria nodorum* also infects the kernels with damage to the grain. Because *S. nodorum* is a seedbome fungus, infected seed is an important source of primary inoculum and can be a more dangerous vehicle of infection for organic farming than in conventional agriculture.

The agronomic, qualitative, and phytopathological aspects concerning National Organic Network of many cultivars of durum and bread wheat have been studied in Italy for some years (Perenzin et al. 2010; Quaranta et al. 2010, Iori et al. 2010). In 2009–10, data collected from field surveys again showed the prevalence of Septoria disease complex on both durum and bread wheats, confirming an increase in the economic importance of this plant disease already observed in recent years. Data related to naturally acquired diseases were reported by Iori et al. (2010).

Our aim was to analyze the behavior of same wheat cultivars at the seedling stage artificially inoculated with *S. nodorum* in greenhouse that were previously observed in field for Septoria disease complex. Seventeen bread wheat and